



# Blast 2 Sequences results

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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

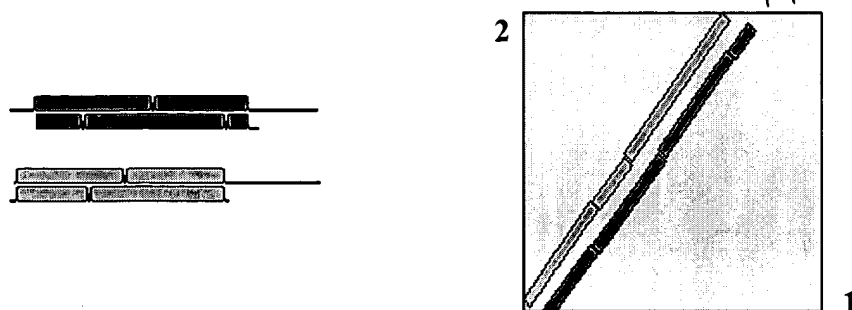
Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

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Sequence 1 lcl|seq\_1 Length 226 (1 .. 226) — Seq No 3  
 Sequence 2 lcl|seq\_2 Length 160 (1 .. 160) — HS FLI

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NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 73.6 bits (179), Expect = 4e-13  
 Identities = 48/155 (30%), Positives = 84/155 (53%), Gaps = 4/155 (2%)

Query: 21 LKNLKEINVGFNYLKSIPPELGDCENLERLDCSGNLELMELPFELSNLKQVTFVDISANK 80  
 L NL ++++ N L +P L +L RL+ S N ++ EL + V +++S N+  
 Sbjct: 1 LSNLADVDLSCNDLTRVPECLYTLPSLRRLNLSSN-QITELSLCIDQVHVETLNLSRNQ 59

Query: 81 FSSVPICVLRMSNLQWLDISSNNLT--DLPQDIDRLEELQSFLLYKNKLTYPYSMLNLK 138  
 +S+P + ++S L+ L ++SN L LP I +L L+ F+ N L +P S+  
 Sbjct: 60 L TSLPSAICKLSKLKKLYLNSNKLD F DGLPSGIGKLTNLEEFMAANNLELVPESLCRCP 119

Query: 139 KL TLLVVGSDHLVELPTALCDSSTPLKFVSLMDNP 173  
 KL LV++ +HLV LP A+ T ++ + + +NP  
 Sbjct: 120 KLRKLVLNKNHLVTLPEAI-HFLTEIEVLVDREN 153

Score = 57.0 bits (136), Expect = 4e-08  
 Identities = 39/153 (25%), Positives = 83/153 (53%), Gaps = 3/153 (1%)

Query: 4 LDLPKNQISHLPAEIGCLKNLKEINVGFNYLKSIPPELGDCENLERLDCSGNLELMELPF 63  
 +DL N ++ +P + L +L+ LN+ N + + + ++E L+ S N +L LP  
 Sbjct: 7 VDLSCNDLTRVPECLYTLPSLRRLNLSSNQITELSLCIDQVHVETLNLSRN-QLTSLPS 65

Query: 64 ELSNLKQVTFVDISANK--FSSVPICVLRMSNLQWLDISSNNLTDLDPQDIDRLEELQSFL 121  
 + L ++ + +++NK F +P + +++NL+ ++NNL +P+ + R +L+ +  
 Sbjct: 66 AICKLSKLKKLYLNSNKLD F DGLPSGIGKLTNLEEFMAANNLELVPESLCRCPKLRKLV 125

Query: 122 LYKNKLTYPYSMLNLKKLTLLVVGSDHLVELP 154

L KN L LP ++ L ++ +L V + + +P  
Sbjct: 126 LNKNHVLVTLP EAIHFLTEIEVL DVRENPNLVMP 158

CPU time:       0.08 user secs.           0.02 sys. secs           0.10 total secs.

Lambda	K	H
0.318	0.136	0.395

Gapped  
Lambda       K       H  
0.267       0.0410    0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 547

Number of Sequences: 0

Number of extensions: 50

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 6

length of query: 160

length of database: 324,428,749

effective HSP length: 107

effective length of query: 53

effective length of database: 107,467,096

effective search space: 5695756088

effective search space used: 5695756088

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 64 (29.3 bits)